RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/517, 939 _____

Source: _____ PCT _____

Date Processed by STIC: _____ 08/22/2005 _____

ENTERED

RAW SEQUENCE LISTING   DATE: 08/22/2005
PATENT APPLICATION: US/10/517,939   TIME: 17:01:01

Input Set : D:\56446-20079.01 - Seqlist (client).txt
Output Set: N:\CRF4\08222005\J517939.raw

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 4 <110> APPLICANT: Steer, Brian
 5        Callen, Walter
 6        Healey, Shaun
 7        Hazlewood, Geoff
 8        Wu, Di
 9        Blum, David
10        Esteghlalian, Alireza
12 <120> TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
13        AND METHODS FOR MAKING AND USING THEM
15 <130> FILE REFERENCE: 564462007901
17 <140> CURRENT APPLICATION NUMBER: 10/517,939
18 <141> CURRENT FILING DATE: 2004-12-13
20 <150> PRIOR APPLICATION NUMBER: PCT/US03/19153
21 <151> PRIOR FILING DATE: 2003-06-16
23 <150> PRIOR APPLICATION NUMBER: 60/389,299
24 <151> PRIOR FILING DATE: 2002-06-14
26 <160> NUMBER OF SEQ ID NOS: 380
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 1128
32 <212> TYPE: DNA
33 <213> ORGANISM: Bacteria
35 <400> SEQUENCE: 1
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37 gccatccagg cccgcctgga gcgcaactgg tatgagatgt cgaaggcccc ggacaagatt     120
38 tactgggaga cgacgaagg cctggggtac gtgatggaca ccggcaacca cgacgtgcgc      180
39 accgagggca tgagctacgc gatgatgatc gccgtgcagt acggccgcaa ggacgtgttc     240
40 gacaagctgt ggggttgggt catgaaatac atgttcatga ccgagggcct gcaccagggc     300
41 tacttcgcct ggtctgtgga ccccagcggc gtaccgaacg ccgacggtcc ggccccggac     360
42 ggcgaggaat acttcgcgat ggacctgttc ctggcctccg cgcgatgggg cgacggcgaa     420
43 ggcgtgtacg agtactcccg ccacgcccgc tcgatcctcc acacctgcgt gcaccagggc     480
44 gaggacggtg aaggctatcc gatgtggaac ccggagaacc atctgatcaa gttcatcccg     540
45 gaaaccgaat ggaccgaccc gtcctaccat ctgccgcact tctacgaggt gttcgccgag     600
46 cgcgccgacg aggccgaccg tccgttctgg gcgcaggccg ccaaggcgag ccgcgagtac     660
47 ctggtcaccg cctgccaccc gcagaccggc atgaaccccg aatactcaaa ctatgatggc     720
48 acgccgcacg tcgacgagcg cgaccactgg catttctact ccgacgccta ccgcaccgcc     780
49 ggcaacatcg gctggactg cctgtggaac ggcgtcgtgc cggaactgtg cgatgcgaat      840
50 gcgcgtctgc agcgtttctt cctcgaacac gaccgcacct gcgtgtatgc gatcgacggc     900
51 acgccggtgg acgagaccgt gctgcacccg gtcggcttca tcgccgccac cgccgaaggc     960
52 tcgctcgccg cgatgcactc gcaggagccg gacgcgctcg acaacgcgat ccgctgggtg    1020
53 cgcctgctgt gggacacccc gatccgcacc ggcacgcgcc gctactacga caacttcctc    1080
54 tacgccttcg cgttcctggc gctggcgggg gagtaccgca cctggtga               1128
56 <210> SEQ ID NO: 2
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59 <213> ORGANISM: Bacteria
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64 Tyr Ser Arg Glu Ala Ile Gln Ala Arg Leu Glu Arg Asn Trp Tyr Glu
65              20                  25                  30
66 Met Phe Glu Gly Pro Asp Lys Ile Tyr Trp Glu Asn Asp Glu Gly Leu
67          35          ,           40                  45
68 Gly Tyr Val Met Asp Thr Gly Asn His Asp Val Arg Thr Glu Gly Met
69      50                  55                  60
70 Ser Tyr Ala Met Met Ile Ala Val Gln Tyr Gly Arg Lys Asp Val Phe
71 65                  70                  75                  80
72 Asp Lys Leu Trp Gly Trp Val Met Lys Tyr Met Phe Met Thr Glu Gly
73              85                  90                  95
74 Leu His Gln Gly Tyr Phe Ala Trp Ser Val Asp Pro Ser Gly Val Pro
75              100                 105                 110
76 Asn Ala Asp Gly Pro Ala Pro Asp Gly Glu Glu Tyr Phe Ala Met Asp
77          115                 120                 125
78 Leu Phe Leu Ala Ser Ala Arg Trp Gly Asp Gly Glu Gly Val Tyr Glu
79      130                 135                 140
80 Tyr Ser Arg His Ala Arg Ser Ile Leu His Thr Cys Val His Gln Gly
81 145                 150                 155                 160
82 Glu Asp Gly Glu Gly Tyr Pro Met Trp Asn Pro Glu Asn His Leu Ile
83              165                 170                 175
84 Lys Phe Ile Pro Glu Thr Glu Trp Thr Asp Pro Ser Tyr His Leu Pro
85              180                 185                 190
86 His Phe Tyr Glu Val Phe Ala Glu Arg Ala Asp Glu Ala Asp Arg Pro
87          195                 200                 205
88 Phe Trp Ala Gln Ala Ala Lys Ala Ser Arg Glu Tyr Leu Val Thr Ala
89      210                 215                 220
90 Cys His Pro Gln Thr Gly Met Asn Pro Glu Tyr Ser Asn Tyr Asp Gly
91 225                 230         .           235                 240
92 Thr Pro His Val Asp Glu Arg Asp His Trp His Phe Tyr Ser Asp Ala
93              245                 250                 255
94 Tyr Arg Thr Ala Gly Asn Ile Gly Leu Asp Cys Leu Trp Asn Gly Val
95              260                 265                 270
96 Val Pro Glu Leu Cys Asp Ala Asn Ala Arg Leu Gln Arg Phe Phe Leu
97          275                 280                 285
98 Glu His Asp Arg Thr Cys Val Tyr Ala Ile Asp Gly Thr Pro Val Asp
99      290                 295                 300
100 Glu Thr Val Leu His Pro Val Gly Phe Ile Ala Ala Thr Ala Glu Gly
101 305                 310                 315                 320
102 Ser Leu Ala Ala Met His Ser Gln Glu Pro Asp Ala Leu Asp Asn Ala
103              325                 330                 335
104 Ile Arg Trp Val Arg Leu Leu Trp Asp Thr Pro Ile Arg Thr Gly Thr
105              340.                345                 350
106 Arg Arg Tyr Tyr Asp Asn Phe Leu Tyr Ala Phe Ala Phe Leu Ala Leu
```

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108 Ala Gly Glu Tyr Arg Thr Trp
109      370              375
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112 <211> LENGTH: 2196
113 <212> TYPE: DNA
114 <213> ORGANISM: Unknown
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Obtained from an environmental sample
119 <400> SEQUENCE: 3
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121 aacaaactgt ttgttaacgg ggtggaatcc ggagataatg ccgaaagaat ctatgtagag     120
122 actggaagcg acatggcgta catccatacc tttgacagca acgacgtgcg ctccgaagga     180
123 atgtcctacg gcatgatgat gtgcgtacag atgaacgatc agacaagatt taacaaactc     240
124 tggaaatggg caagaaccta tatgtacaat gaaacagacg ccggcagtaa ttccaggggc     300
125 tatttctcat ggcagtgcag tacaagcggc tcaaaaatgg ataagggccc cgctcctgac     360
126 ggcgaggaat actttattac ggcgctgttg ttcgcgcacg cccgctgggg gagcgcgtcc     420
127 ggtactacaa acataaacaa ttacgcgcag caagcaaggc agattatcta tgacttaacg     480
128 cgccgcaaac cggggaacgg agatccttac ggcgagcctt caatgtttaa tgtagacaac     540
129 tatatggtta gattcgccac acttggaaat tccgccacct ttacagaccc ctcataccat     600
130 ttaccggcat tctatgatgt ttgggcgctg gaattacagg cggactatga taatagtaaa     660
131 ctctacggta tctgggctga taaggctgac ttgaaaaaag acattgatta ctttaaacaa     720
132 gcggcgacca caagccgttc attctttgca aaaacgacaa acggtacaac cggacttgga     780
133 ccggattatg ccggctttga cggaacgcct aaaaatgaag gggatcacaa gtatttcgag     840
134 tatgacgcgt ggcgtatcgc gatgaacata ggtatggact acgcgtggtt cgcgaaagat     900
135 tcctggcaga agacatttgc cgacagaatt caggcgttct ttgtcagcaa gggagtcact     960
136 tcttacggaa accgctggac attggacggg actcaaaggg gagcggatca ctcgccgggt    1020
137 cttgtcggct gtaacgcggt cgcctctctc gcggcgacaa acgcgaacgc gtggaaattt    1080
138 atcgaagact tctggaacat cagcatgacg aaaggcaaat accgttacta tgacggatgt    1140
139 ctgtatatga tgagcatgct gcacttaagc ggcaacttta aggcgtatct ttctacaaat    1200
140 accacgcccg ccaacagttc cagcattacc ccgacaaccg cgtctttcga caagaagaca    1260
141 agcgcacaag ccgacattgc cgtaacagtg acgcttaacg ggaatacatt ctcaagtatc    1320
142 acaaacaacg gtacagccct tacaagcggc acagactact cagtgagtgg aacaaagtat    1380
143 acgataaaga aagaatacct tgcaaaacag cctgtaggaa caacgaagct cgcattcaac    1440
144 ttcagtgccg gaggaactcc ggaacttaca gttactataa cggacacggg cagctccagc    1500
145 atcagcccga caaccgcgac attcgacaaa aagaccggag cgcaagccga catcgccgta    1560
146 accatgacgc ttaatgggaa tactttgtcg aacatcaaaa acggttctgc acaacttaca    1620
147 agcggaactg actactcaac gagcggcagt acggtaacga ttaaaaaaga atacctggca    1680
148 aagcaggcta acggcacagt aacgcttacc ttcacattca gcgcaggcgc ggcccaaact    1740
149 attgacatca cggtaaaaga tacaaccggc ggagcggcgg aataaaata caacttcgca    1800
150 actgacaacc tgcccaacgg gtacccgaag tacagttcaa gtgatatatc cgcgacaata    1860
151 accggaggag ctttggtaat aaccaaaacc ggaaataatt cgtccccgaa gattacattg    1920
152 ccctttagtg taacaggtaa cctttccggt tatacaggca taaagataaa tgtaaaggga    1980
153 gtatccggag atttcactta taaagtattg aatgccgcaa taggttctac aaatctcggc    2040
154 agcgtaaata acgccccaat accaaacggc tcatttggag acgtaacaat accaataacc    2100
155 ggcggtacaa acaccggaga tttagatata tcgttctggc tcaataacac aaatgcttac    2160
156 gttattgaga ttaagagcat agagctggta aaatga                                2196
158 <210> SEQ ID NO: 4
159 <211> LENGTH: 711
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160 <212> TYPE: PRT
161 <213> ORGANISM: Unknown
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Obtained from an environmental sample
166 <400> SEQUENCE: 4
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168 1               5                   10                  15
169 Asn Thr Ala Trp Asn Lys Leu Phe Val Asn Gly Val Glu Ser Gly Asp
170             20                  25                  30
171 Asn Ala Glu Arg Ile Tyr Val Glu Thr Gly Ser Asp Met Ala Tyr Ile
172         35                  40                  45
173 His Thr Phe Asp Ser Asn Asp Val Arg Ser Glu Gly Met Ser Tyr Gly
174     50                  55                  60
175 Met Met Met Cys Val Gln Met Asn Asp Gln Thr Arg Phe Asn Lys Leu
176 65                  70                  75                  80
177 Trp Lys Trp Ala Arg Thr Tyr Met Tyr Asn Glu Thr Asp Ala Gly Ser
178             85                  90                  95
179 Asn Ser Arg Gly Tyr Phe Ser Trp Gln Cys Ser Thr Ser Gly Ser Lys
180             100                 105                 110
181 Met Asp Lys Gly Pro Ala Pro Asp Gly Glu Glu Tyr Phe Ile Thr Ala
182         115                 120                 125
183 Leu Leu Phe Ala His Ala Arg Trp Gly Ser Ala Ser Gly Thr Thr Asn
184     130                 135                 140
185 Ile Asn Asn Tyr Ala Gln Gln Ala Arg Gln Ile Ile Tyr Asp Leu Thr
186 145                 150                 155                 160
187 Arg Arg Lys Pro Gly Asn Gly Asp Pro Tyr Gly Glu Pro Ser Met Phe
188             165                 170                 175
189 Asn Val Asp Asn Tyr Met Val Arg Phe Ala Thr Leu Gly Asn Ser Ala
190             180                 185                 190
191 Thr Phe Thr Asp Pro Ser Tyr His Leu Pro Ala Phe Tyr Asp Val Trp
192         195                 200                 205
193 Ala Leu Glu Leu Gln Ala Asp Tyr Asp Asn Ser Lys Leu Tyr Gly Ile
194     210                 215                 220
195 Trp Ala Asp Lys Ala Asp Leu Lys Lys Asp Ile Asp Tyr Phe Lys Gln
196 225                 230                 235                 240
197 Ala Ala Thr Thr Ser Arg Ser Phe Phe Ala Lys Thr Thr Asn Gly Thr
198             245                 250                 255
199 Thr Gly Leu Gly Pro Asp Tyr Ala Gly Phe Asp Gly Thr Pro Lys Asn
200             260                 265                 270
201 Glu Gly Asp His Lys Tyr Phe Glu Tyr Asp Ala Trp Arg Ile Ala Met
202             275                 280                 285
203 Asn Ile Gly Met Asp Tyr Ala Trp Phe Ala Lys Asp Ser Trp Gln Lys
204     290                 295                 300
205 Thr Phe Ala Asp Arg Ile Gln Ala Phe Phe Val Ser Lys Gly Val Thr
206 305                 310                 315                 320
207 Ser Tyr Gly Asn Arg Trp Thr Leu Asp Gly Thr Gln Arg Gly Ala Asp
208             325                 330                 335
209 His Ser Pro Gly Leu Val Gly Cys Asn Ala Val Ala Ser Leu Ala Ala
210             340                 345                 350
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211 Thr Asn Ala Asn Ala Trp Lys Phe Ile Glu Asp Phe Trp Asn Ile Ser
212         355             360             365
213 Met Thr Lys Gly Lys Tyr Arg Tyr Tyr Asp Gly Cys Leu Tyr Met Met
214         370             375             380
215 Ser Met Leu His Leu Ser Gly Asn Phe Lys Ala Tyr Leu Ser Thr Asn
216 385             390             395                 400
217 Thr Thr Pro Ala Asn Ser Ser Ser Ile Thr Pro Thr Thr Ala Ser Phe
218             405             410             415
219 Asp Lys Lys Thr Ser Ala Gln Ala Asp Ile Ala Val Thr Val Thr Leu
220         420             425             430
221 Asn Gly Asn Thr Phe Ser Ser Ile Thr Asn Asn Gly Thr Ala Leu Thr
222         435             440·            445
223 Ser Gly Thr Asp Tyr Ser Val Ser Gly Thr Lys Tyr Thr Ile Lys Lys
224         450             455             460
225 Glu Tyr Leu Ala Lys Gln Pro Val Gly Thr Thr Lys Leu Ala Phe Asn
226 465             470             475                 480
227 Phe Ser Ala Gly Gly Thr Pro Glu Leu Thr Val Thr Ile Thr Asp Thr
228             485             490             495
229 Gly Ser Ser Ser Ile Ser Pro Thr Thr Ala Thr Phe Asp Lys Lys Thr
230         500             505             510
231 Gly Ala Gln Ala Asp Ile Ala Val Thr Met Thr Leu Asn Gly Asn Thr
232         515             520             525
233 Leu Ser Asn Ile Lys Asn Gly Ser Ala Gln Leu Thr Ser Gly Thr Asp
234         530             535             540
235 Tyr Ser Thr Ser Gly Ser Thr Val Thr Ile Lys Lys Glu Tyr Leu Ala
236 545             550             555                 560
237 Lys Gln Ala Asn Gly Thr Val Thr Leu Thr Phe Thr Phe Ser Ala Gly
238             565             570             575
239 Ala Ala Gln Thr Ile Asp Ile Thr Val Lys Asp Thr Thr Gly Gly Ala
240         580             585             590
241 Ala Gly Ile Lys Tyr Asn Phe Ala Thr Asp Asn Leu Pro Asn Gly Tyr
242         595             600             605
243 Pro Lys Tyr Ser Ser Ser Asp Ile Ser Ala Thr Ile Thr Gly Gly Ala
244         610             615             620
245 Leu Val Ile Thr Lys Thr Gly Asn Asn Ser Ser Pro Lys Ile Thr Leu
246 625             630             635                 640
247 Pro Phe Ser Val Thr Gly Asn Leu Ser Gly Tyr Thr Gly Ile Lys Ile
248             645             650             655
249 Asn Val Lys Gly Val Ser Gly Asp Phe Thr Tyr Lys Val Leu Asn Ala
250         660             665             670
251 Ala Ile Gly Ser Thr Asn Leu Gly Ser Val Asn Asn Ala Pro Ile Pro
252         675             680             685
253 Asn Gly Ser Phe Gly Asp Val Thr Ile Pro Ile Thr Gly Gly Thr Asn
254         690             695             700
255 Thr Gly Asp Leu Asp Ile Ser
256 705             710
258 <210> SEQ ID NO: 5
259 <211> LENGTH: 2106
260 <212> TYPE: DNA
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VERIFICATION SUMMARY   DATE: 08/22/2005
PATENT APPLICATION: US/10/517,939   TIME: 17:01:02

Input Set : **D:\56446-20079.01 - Seqlist (client).txt**
Output Set: **N:\CRF4\08222005\J517939.raw**

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L:312 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:315 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:449 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:452 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:558 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
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L:837 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
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L:1095 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1098 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
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L:1188 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1355 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
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L:3185 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:58
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L:3670 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:68
L:3769 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3772 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:70
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L:4034 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:74
L:4259 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
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L:4660 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:84
L:4914 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
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L:5527 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:100
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L:5615 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:102
L:5708 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5709 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!
L:5840 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5843 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:106
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L:6619 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:120
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L:7525 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:136
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L:8377 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:152
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L:8560 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:8563 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:156
L:8672 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:8675 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:158
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Input Set : **D:\56446-20079.01 - Seqlist (client).txt**
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L:8741 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
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L:8829 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:162
L:8914 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:164
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